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CDC20, a cofactor of the APC complex, should be responsible for a short-petiole trait in soybean [*Glycine max* (L.) Merr.]

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Short petiole is potentially useful to improve soybean yields by altering the soybean canopy profile and increasing planting density. Though the petiole length of a plant is changeable by photoperiod and light quality, distinctively short petioles are heritable and therefore can be used in breeding. *Sp* is a recombinant soybean short-petiole mutant with a normal pulvinus and a dwarf phenotype. Genetic investigations indicate that the short-petiole trait is caused by at least two recessive genes. Map-based cloning identified one locus, *sp1*, as cell division cycle 20, a cofactor of the APC complex, which is an essential regulator of cell division. The *sp1* locus was mapped to chromosome 11 using two different F₂ populations. Based on sequence analysis among NILs, a substitution has been found in the candidate gene for *sp1*, which results in an amino acid change from leucine to valine in CDC20 protein. To verify the gene function of *sp1*, CRISPR-Cas9 vectors with two different gRNA targeting CDC20 has been transformed into hairy roots and somatic embryos via agrobacterium-mediated transformation and gene gun bombardment, respectively. Hairy root transgenic analysis show that hairy root genome indeed has been edited which means gRNA sequences designed for CRISPR-Cas9 system should be effective in soybean plant. Collectively, these results indicate that the gene which encodes the CDC20 protein should be the candidate for the *sp1* locus, and the CDC20 protein family should play an important role in dwarf phenotypes and shortening leaf petioles. Further validation of gene function via somatic transformation is being done in soybean using CRISPR-Cas9 technology to create independent knock-out alleles.